RAW SEQUENCE LISTING
ERROR REPORT

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)**
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Revised 01/29/2002
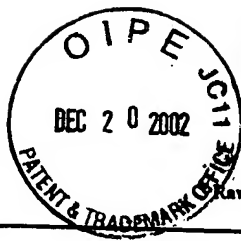
Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10 045,574

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1___✓___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3__✓__ Misaligned Amino
Numbering

The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____ Skipped Sequences
(OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)　　SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)　(Sec. 1.823 of Sequence Rules)

12_____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

SEQUENCE LISTING

<110> MACKAY, Fabienne
      KALLED, Susan

<120> BAFF, Inhibitors Thereof and Their Use
      in the Modulation of B-Cell Response and
      Treatment of Autoimmune Disorders

<130> 08201.0024-01000

<140> 10/045,574

<141> 2001-11-07

<150> 60/117,169

<151> 1999-01-25

<150> 60/143,228

<151> 1999-07-09

<150> PCT/US00/01788

<151> 2000-01-25

<150> 09/911,777

<151> 2001-07-24

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 218
<212> PRT
<213> Homo Sapien

<400> 1

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Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro
            20                  25                  30
Arg Lys Glu Ser Pro Ser Val Leu Leu Ser Cys Cys Leu Thr Val Val
            35                  40                  45
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
        50                  55                  60
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Lys
65                  70                  75                  80
Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser
                85                  90                  95
Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln Asp
            100                 105                 110
Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly
        115                 120                 125
Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala
    130                 135                 140
Leu Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His
145                 150                 155                 160
Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
                165                 170                 175
Val Thr Leu Phe Arg Cys Ile Gln Asn Leu Glu Glu Gly Asp Glu Leu
            180                 185                 190
Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp
        195                 200                 205
Val Thr Phe Phe Gly Ala Leu Lys Leu Leu
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<210> 2
<211> 232
<212> PRT
<213> Murine

<400> 2

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Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
            20                  25                  30
Gln Lys Glu Glu Gly Ala Val Leu Leu Ser Ser Ser Phe Thr Ala Met
        35                  40                  45
Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu Arg
        50                  55                  60
Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala Lys
65                  70                  75                  80
Leu Leu Thr Pro Ala Ala Pro Arg Pro His Asn Ser Ser Arg Gly His
                85                  90                  95
Arg Asn Arg Arg Ala Phe Pro Gly Pro Glu Glu Thr Glu Gln Asp Val
            100                 105                 110
Asp Leu Ser Ala Pro Pro Ala Leu Arg Asn Ile Ile Gln Asp Cys Leu
            115                 120                 125
Gln Leu Ile Ala Asp Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr
    130                 135                 140
Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Tyr
145                 150                 155                 160
Ser Gln Val Leu Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile
                165                 170                 175
Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
            180                 185                 190
Leu Phe Arg Cys Ile Gln Asn Leu Glu Glu Gly Asp Glu Ile Gln Leu
            195                 200                 205
Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr
    210                 215                 220
Phe Phe Gly Ala Leu Lys Leu Leu
225                 230
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<210> 3
<211> 102
<212> PRT
<213> Homo Sapien

<400> 3

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1               5                   10                  15
Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys
            20                  25                  30
Arg Gly Ser Ala Leu Glu Glu Lys Tyr Gly Gln Val Leu Tyr Thr Asp
        35                  40                  45
Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val His Val
    50                  55                  60
```

Phe Gly Asp Glu Leu Ser Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala
65   70   75   80
Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn
                85   90   95
Ala Gln Ile Ser Leu Asp
            100

<210> 4
<211> 96
<212> PRT
<213> Homo Sapien

<400> 4

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Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
                20   25   30
Gly Arg Gly Leu Gln Ala Gln Tyr Ser Gln Val Leu Phe Gln Asp Val
            35   40   45
Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Ala
        50   55   60
Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp
65   70   75   80
Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser
                85   90   95

<210> 5
<211> 104
<212> PRT
<213> Homo Sapien

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                20   25   30
Val Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
            35   40   45
Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
        50   55   60

Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly
65   70   75   80
Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg
                85   90   95
Pro Asp Tyr Leu Asp Phe Ala Glu
            100

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<212> PRT
<213> Homo Sapien

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Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly
            20   25   30
Val Lys Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu
        35   40   45
Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Met
    50   55   60
Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
65   70   75   80
Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
                85   90   95
Glu

<210> 7
<211> 102
<212> PRT
<213> Homo Sapien

<400> 7

Thr Leu Lys Pro Ala Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn
1   5   10   15
Ser Leu Leu Trp Arg Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly
            20   25   30
Phe Tyr Ser Gln Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala
        35   40   45

Thr Ser Ser Pro Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser
    50   55   60
Gln Tyr Pro Phe Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe
65   70   75   80
Gln Leu Thr Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro
                85   90   95
His Leu Val Leu Ser Phe
            100

<210> 8
<211> 109
<212> PRT
<213> Homo Sapien

<400> 8

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                20   25   30
Trp Gly Lys Ile Ser Asn Met Tyr Ala Asn Ile Cys Phe Arg His His
            35   40   45
Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr
    50   55   60
Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Glu Phe His Phe Tyr Ser
65   70   75   80

Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser
                85   90   95
Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
            100   105

<210> 9
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<213> Homo Sapien

<400> 9

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<213>  Homo Sapien

<400>  10

gacaagcttg ccaccatgga tgactccaca                                30



<210>  11
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<212>  DNA
<213>  Homo Sapien

<400>  11

actagtcaca gcagtttcaa tgc                                       23



<210>  12
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<212>  DNA
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<400>  12

ctgcagggtc cagaagaaac ag                                        22



<210>  13
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<400>  13

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<400> 21

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<210> 22
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<213> Homo Sapien

<400> 22

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